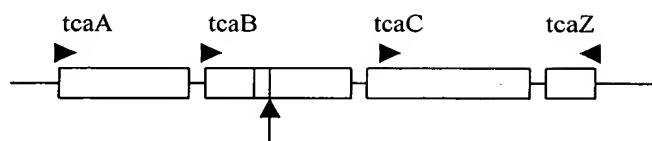
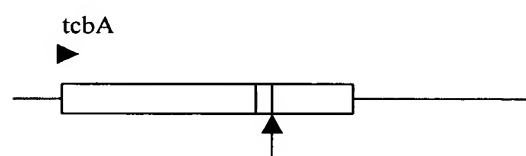


Photorhabdus

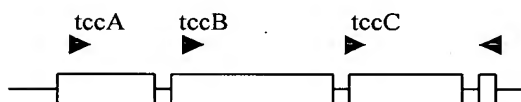
tca



tcb



tcc



tcd

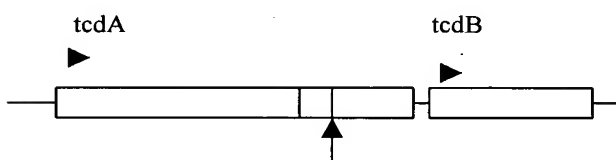


FIG. 1

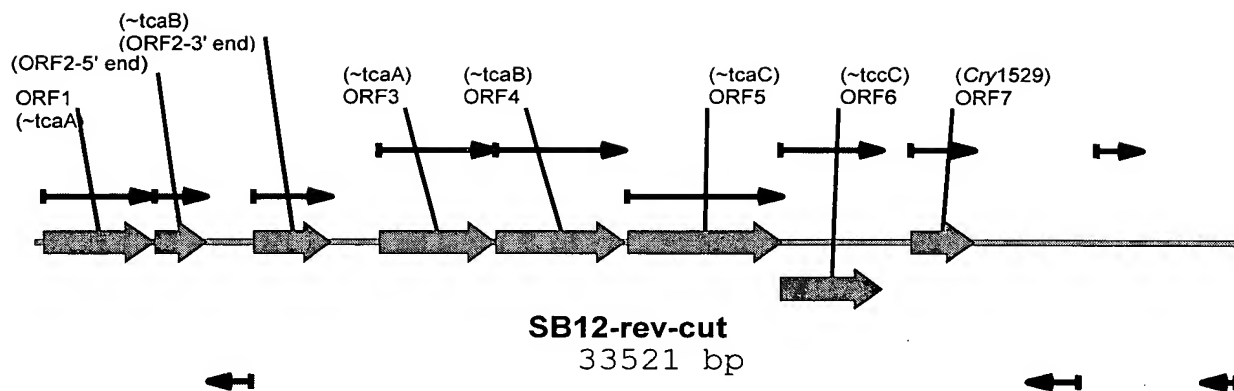


Fig. 2

2THIA

or

AAC44156: DITLKVAIYPYVPDPARFQA

|||||

SEQ ID NO:17: DITLKVAIYPYVPDPSRFQA

Fig. 3

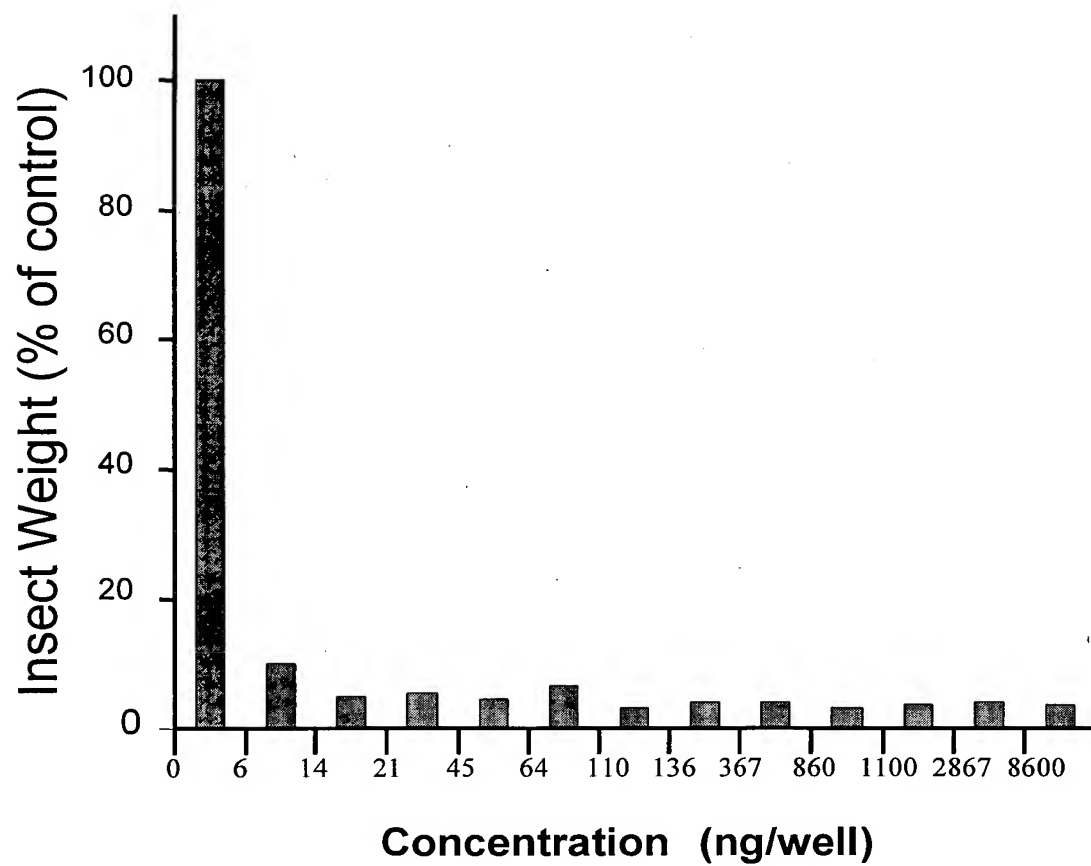


Fig. 4

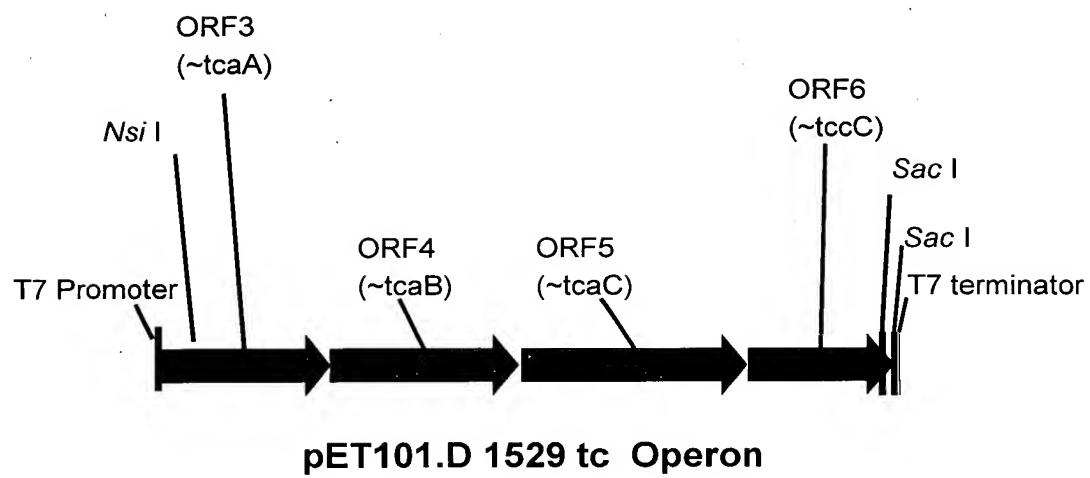


Fig. 5

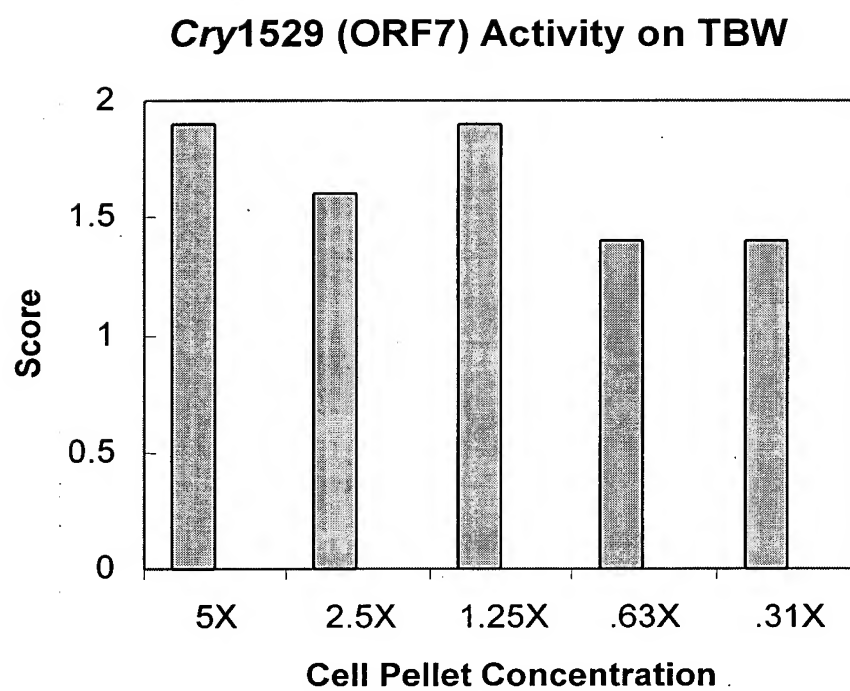


Fig. 6

SEQ ID NO:9(top) x SEQ ID NO:5(bottom)

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1  MTKEGDKHMSTSTLLQSIKEARRDALVNHYIANQVPTALADKITDADSLY  50
   |||||:|:||||||| || | ||||| || | |||||
1  MTKEGGKNMSTSTLLQLIKESRRDALVNHYIANNVPRELTDKITDADSLY  50

51  EYLLLDTKISELVKTSPIAEAISSVQLYMNRCVEGYEGKLTPESENTHFGP  100
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51  EYLLLDTKISELVKTSPIAEAISSVQLYMNRCVEGYEGKLTPEGNSHFGP  100

101 GKFLYNWDTYNKRFTWAGKERLKYAGSYIEPSLRYNKTDPPFLNLEQSI  150
   ||||:||||||| ||||| ||||| ||||| ||||| |||||
101 GKFLNNWDTYNKRFTWAGKERLKYAGSYIDPSLRYNKTDPPFLNLEQNI  150

151 SQGRITDDTVKNALQHLYLTEYEVLADLDYISVNKGGDESVLLFVGRTKTV  200
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 SQGRITDDTVKNALQHLYLTEYEVLADLEYISVNKGADSVLFFVGRTKTM  200

201 PYEYWRRLLLKRDNNNNKLVPAVWSQWKKISANIGEAVDSYVVPRWKHNR  250
   ||||| ||:||||||| ||||| |||||:| || :|:|
201 PYEYWRRLTLKKDNNNNKLVPAIWSQWKKITANIGEAVNNYVVLHWHNNR  250

251 LHVQWCSIEKSENDAGEPIEKRYLNDWFMDSSGVWSSFRKIPVVEKSFEY  300
   |||| | || |:||||||| |||||:|:||||| :|:|
251 LHVQWGSTEKTQNDGGEPIEKRYLNDWFMDKSSVWSSFRKVSYIENSFTY  300

301 LDGSLDPRFVALVRNQILIDEPEIFRITVSAPNPIDANGRVEVHFEENYA  350
   | | | :| | | | :| | | | :| :| :|
301 TEGIIDSRNITIAGNQFCDDSNFTKATITA.LPFDQIRVYLEKIYGTGG  349

351 NRYNITIKYGTTSIAIPAGQVGHPNISINETLRVEFGTRPDWYYTFRYLG  400
   : : : :| :| :| :| :| :| :| :| :|
350 SITVTGENKGYIIVKGEPREVSFSPNTLLDVFIGSNASPRDPYFKATFNR  399

401 NTIQNSYGSIVNNQFSPPSGSNIKGPIDLTLKNNIDLSALLDES LDALFD  450
   |||||: || ||||| ||||| ||||| ||||| |||||
400 EALQNSYGSIKINQYTPPSGSNIKGPIDLTLKNNIDLSALLEESLDVLF  449

451 YTIQGDNLGGLAAFNGPYGLYLWEIFFHVPFLMAVRFHTE--QRYELAERW  500
   |||||:||||| ||||| ||||| ||||| ||||| |||||
450 YTIQGNNQLGGLAAFNGPYGLYLWEIFFLHVPFLMAVRFHTE] [QRYELAERW  499

501 FKFIFNSAGYRDDYGSLLTDDKGNVRYWNVIPLQEDTEWDDTLSLATTD  550
   |||||:|:||||||| ||||| ||||| ||||| |||||
500 FKFIFNSAGYRDGYGNLLTDDKGNVRYWNVVPLQEDTEWDDTLSLATTD  549

551 DEIAMADPMQYKLAIFIHTMDFLISRGDSLYRMLERDTLAEAKMYIIQAS  600
   ||||| ||||| ||||| ||||| ||||| ||||| |||||
550 DEIAMADPMQYKLAIFIHTLDFLISRGDSLYRMLERDTLTEAKMYIIQAS  599

601 QLLGPRPDIRLNHWPNTLQSEADAVTAVPTRSDSPAAPILALRALLTG  650
   ||||| || |||||:||||||| ||||| ||||| |||||
600 QLLGPRPEIRINHWPDPNTLQSEADAVTAVPTRSDSPAAPILALRALLNA  649

```

Fig. 7A

651	ENGHFLPPYNDELFAFWDKIDRLRLYNLRHNLSLDGGQPLHLPLFAEPVNP	700
650	ENGHFLPPYNDELLAFWDKIDRLRLYNLRHNLSDGGQPLHLPLFTEPVNPR	699
701	ELQVQHGP GDGLGGSAGSAQSRQSVYRFPLVIDKARNAANSVIQFNALE	750
700	ELQVQHAGDGLGGSAGSVQSRQSVYRFPLVIDKARNAASSVIQFNALE	749
751	NALTQKDSEAMTMLLQSQQQIVLQQTRDIQEKNLAALQASLEATMTAKAG	800
750	NALTQKDSEAMTMLLQSQQQIVLQQTRDIQEKNLASLQASLEATMTAKAG	799
801	AESRKTHFAGLADNWMSDNETASLALRTTAGIINTSSSTVP IAITGGLDMA	850
800	AKSRKTHFAGLADNWM SHNETASLALRTTAGIINTSSSTVP IAITGGLDMA	849
851	PNIFGFVGGSRWGAASAAVAQGLQIAAGVMEQTANIIDISESYRRRRED	900
850	PNIFGFVGGSRWGAASAAVAQGLQIAAGVMEQTANIIDISESYRRRRED	899
901	WLLQRDVAENEAQLDSQIAALREQMDMARKQLALAETEQAHAQAVYELQ	950
900	WLLQRDVAENEAQLDSQIAALREQMDMARKQLALAETEQAHAQAVYELL	949
951	STRFTNQALYNWMAGRLSSLYYQMYDAALPLCLMAKQALEKEIGSDKTVG	1000
950	STRFTNQALYNWMAGRLSSLYYQMYDAALPLCLMAKQALEKEIGNDKTVG	999
1001	VLSLPAWNDLYQGLLAGEALLLELQKLENLWLEEDKRGMEAVKTVSLDTL	1050
1000	IFTLPAWNDLYQGLLAGEALLLELQKLENLWLEEDKRGMEAVRTVSLDTL	1049
1051	LRKTNPNSGFADLVKEALDENGKTPDPVSGVGVQLQNNIFSATLDLSVLG	1100
1050	LRKEKPESGFADLVK. EVLDGKTPDPVSGVSVQLQNNIFSATLDLSTLG	1097
1101	LDRSYNQA EKSRRIKNMSVTLPALLGPYQDIEATLSLGGETVALSHGVDD	1150
1098	LDRFYNQA EKAHRIKNLSVTLPALLGPYQDIAATLSLGGETVALSHGVDD	1147
1151	SGLFITDLNDSRFLPFEGMDPLSGTLVLSIFHAGQDGDQRLLESNDVI	1200
1148	SGLFITDLNDSRFLPFEGMDPLSGTLVLSILHAGQDGDQRLLESNDVI	1197
1201	FHIRYVMK* 1209	
1198	FHIRYVMK* 1206	

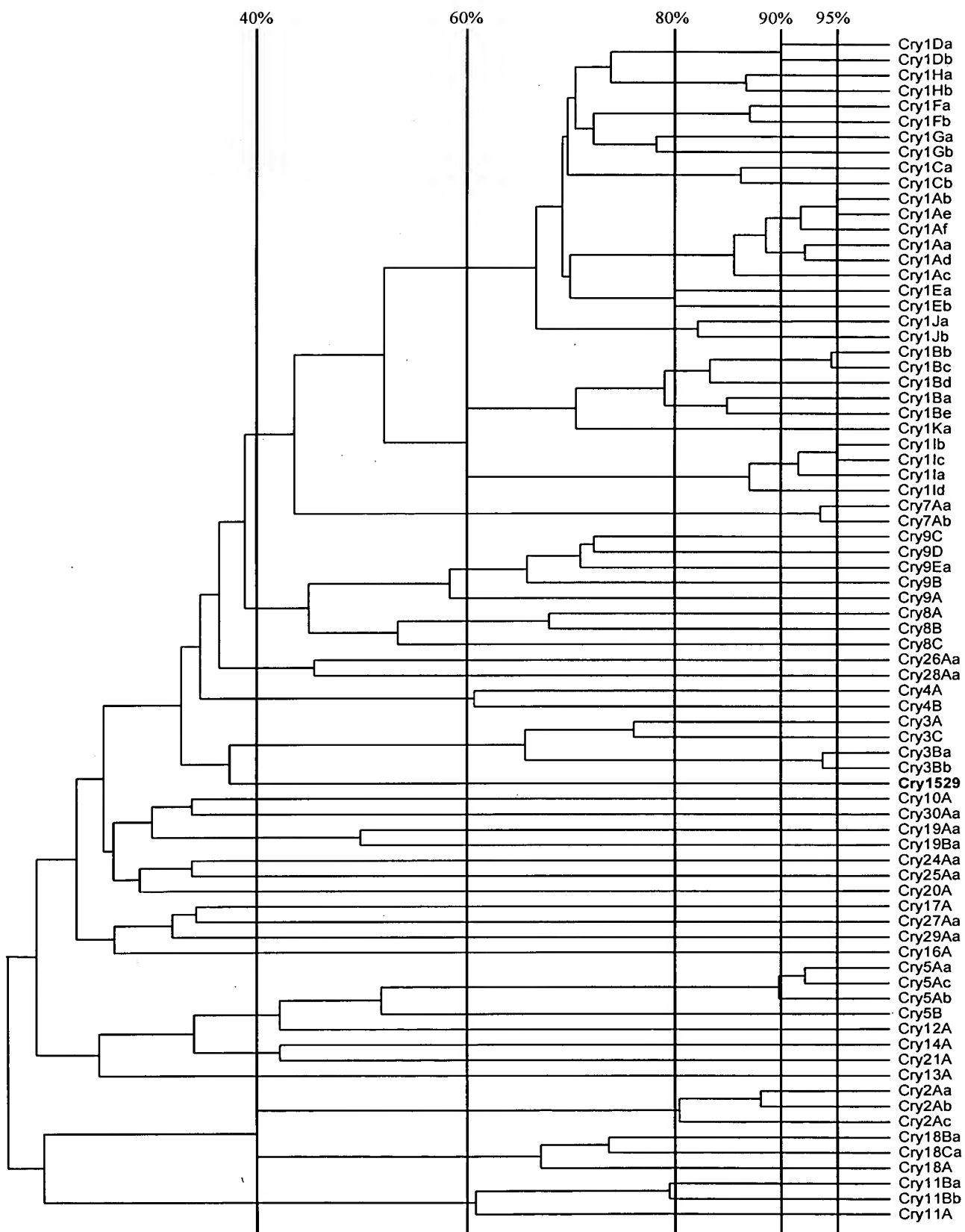


Fig. 8.

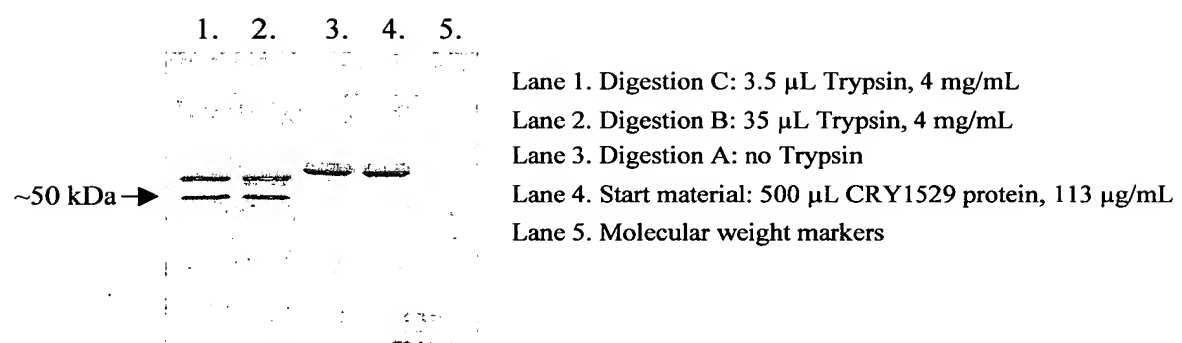


FIG. 9

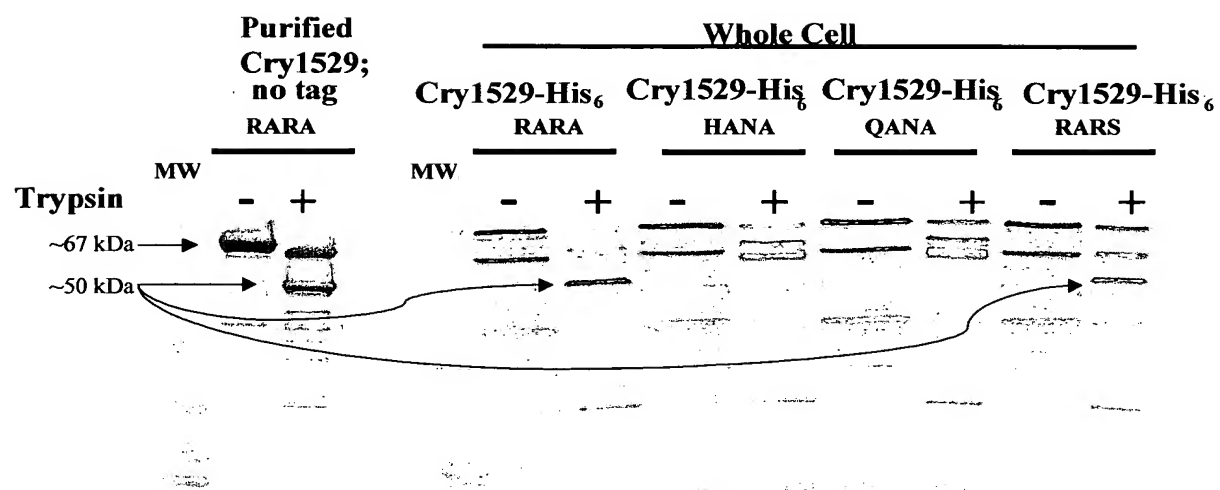


Fig. 10

		501		550
tcaA2-1529	(500)	AGTCGCTGATCCTCAATAATGACAATATGAACCGAGAGGTAT	CTTCTCTG	
tcaA1-1529	(485)	AGTCGCTGATCCTCAATAATGACAATATGAACCGTGAGGTGT	CTTCCCTG	
tcaA-W14	(485)	AGGATCTGATATTAAGCGAAACGACGATGAATAAAGAGGTCA	CTTCCCTT	
		551		600
tcaA2-1529	(550)	GATATCCTTCTGGATGTGCT	GCAGCCCGAAGGCTCTGACACGCTGACATC	
tcaA1-1529	(535)	GATATCCTGCTGGATGTGCT	GCAGTCCGAAGGCTCCGGCACACTGACATC	
tcaA-W14	(535)	GATATCTTGTGGATGTGCT	ACAAA--AAGGCGGTAAAGATATTACTGA	
SB105				

Fig. 11A

		1901		1950
tcaA2-1529	(1824)	GATGCGCAGCACGGGTCTTTCCTTTGAGCAG	TTGGATTGGCTGATTGCCA	
tcaA1-1529	(1788)	GGCGCGCAGCACGGGACTTTCCTTTGAGCAG	TTGGATTGGCTGATTACCA	
tcaA-W14	(1809)	ATCATCCCAGACCGGGCTATCATTGAAGAA	TTGGACTGGCTGATTGCCA	
SB106				
		1951		2000
tcaA2-1529	(1874)	ATGCCAGCCGT	GCCGTTATCGAACACGGTGGAGAGCTTTTTCTGGATAAG	
tcaA1-1529	(1838)	ATACCAGCCGT	GCCGTAATCGAACATGGTGGAGAACTGATTCTGGATAAG	
tcaA-W14	(1859)	ATGCCAGTCGT	AGTGTGCCGGACCACCACGACAAAATTGTGCTGGATAAG	

Fig. 11B

		1651		1700
tcaB2-1529	(1611)	GGAGTGGGATGACACGTTGTCCCTGGCAACGACCGACCCGGACGAGATT		G
tcaB-W14	(1557)	CGCATGGGATACCACACAGCCC--GCCACCACTGATCCAGATGTGATC		G
tcaB1-1529	(1608)	GGAGTGGGATGACACGTTGTCCCTGGCAACGACCGACCCGGACGAGATT		G
		1701		1750
tcaB2-1529	(1661)	CGATGGCCGACCCGATGCAATACAAGCTGGC	TATATTTATT	CACACCATG
tcaB-W14	(1604)	CTATGGCGGACCCGATGCATTACAAGCTGGC	GATATTCCTGC	TACCCTT
tcaB1-1529	(1658)	CGATGGCCGACCCGATGCAATACAAGCTGGC	TATCTTTATT	CACACCTTG

SB101

Fig. 12A

		2051		2100
tcaB2-1529	(1999)	TGGGACAAAATCGATCTGCGTTTATACAATTTG	CGCCACAATTTGAGTCT	
tcaB-W14	(1951)	TGGGATAAACTTGAGTTACGCCTATACAACCTG	CGCCACAATCTGAGTCT	
tcaB1-1529	(1996)	TGGGATAAAATCGACCTGCGTCTCTACAATTTA	CGCCACAATCTGAGCCT	
SB102				
		2101		2150
tcaB2-1529	(2049)	GGACGGTCAGCCGCT	TCATTTGCCGCTCTTTGCCGAACCGGTCAATCCG	C
tcaB-W14	(2001)	GGATGGTCAACCGCT	AAATCTGCCACTGTATGCCACGCCGGTAGACCCGA	
tcaB1-1529	(2046)	GGACGGTCAGCCGCT	TCATTTGCCGCTCTTTACCGAACCGGTCAATCCTC	

Fig. 12B

		2901		2950
tcaB2-1529	(2845)	CTGCAAAGCACCCGCTTTACGAATCAAGCTT	TGTATAACTGGATGGCTGG	
tcaB-W14	(2797)	CTGCAAACCACTCGTTTTACCGGGCAGGCAC	TGTATAACTGGATGGCCGG	
tcaB1-1529	(2842)	CTGCTAAGCACCCGTTTTACGAATCAAGCTT	TGTATAACTGGATGGCCGG	
SB103				
		2951		3000
tcaB2-1529	(2895)	ACGTCTGTC	GTCTCTATACTATCAAATGTATGACGCCGCATTGCCGCTCT	
tcaB-W14	(2847)	TCGTCTCTC	CGCGCTCTATTACCAAATGTATGATTCCACTCTGCCAATCT	
tcaB1-1529	(2892)	ACGTCTGTC	GTCTCTATACTATCAAATGTATGACGCCGCATTGCCGCTCT	

Fig. 12C

		2201		2250
tcaC-1529	(2125)	AGCTCGTTTTGGTAC	CGAAGCTCCACCCAGTATTGGCTGGATGAGAAA	CA
tcdB1-W14	(2149)	CACACCTTGCATTAC	CGTAGCTCTGTCCAGTTCTGGCTGGATGAAAAA	GC
tcdB2-W14	(2128)	CACACCTTGCATTAC	CGCAGTTCCTCCCAATTCTGGCTGGATGAAAAA	GC
xptC1-Xwi	(2188)	ACCACGCTGTATTAT	CGCAGCTCTGCCCAGTTCTGGCTGGATGAGAAA	TT

SB215

Fig. 13A

		4501		4550
tcaC-1529	(4263)	ATGGGTTTACAGTAAACGAAGATGAAAATGATAC	CATGGACTCATCATTAT	
tcdB1-W14	(4380)	GTGGTTTACCGTGAGTGAGGATGAGAATGATAC	GGCCG-CTGATGCGCTG	
tcdB2-W14	(4362)	CTGGTTTACTGTCAATGAAGATGAAAATGACAC	AGCCG-CTGAGGTGAAG	
xptC1-Xwi	(4428)	CTGGTTTGTGGTGAATGAAGATGAAAATGACAC	TGCCG-GTGAAATGACA	

SB217

Fig. 13B

		1051		1100
tccC-1529	(1027)	TAT	CGTTATGAATATGATCCGGTAGGCAAT	ATCCTTTCTATTTACAATGA
tccC1-W14	(973)	CTA	CGCTATAAGTATGATCCGGTGGGGAAT	GTTATCAGTATCCATAATGA
tccC2-W14	(940)	TTA	CGCTATCAATATGACCCGGTAGGCAAT	GTGATCAATATCCGTAATGA
tccC3-W14	(961)	CTG	CGCTATGAATATGACCCGGTAGGCAAT	GTCATCAGCATCCGTAATGA
tccC4-W14	(961)	CTA	CGCTATGAACATGATCCTGTAGGGAAT	ATTATTAGTGTCCGTAATGA
tccC5-W14	(955)	CTA	CGCTATCAATATGACCCAGTAGGCAAT	GTCATTAGTATCCGTAATGA
xptB1-Xwi	(973)	CTG	CGTTATGAATATGATCCTGTCGGAAT	GTGCTGAAATCAACTAATGA

SB212

Fig. 14A

		1951		2000
tccC-1529	(1903)	TACAAGACCATC	CGCTATTTCAGGCAAAGAGCGGGATG	CCACAGGCCTGTA
tccC1-W14	(1861)	TACAAATTTATT	CGTTACTCCGGTAAAGAGCGGGATG	CCACTGGATTGTA
tccC2-W14	(1807)	TATAAAACGATT	CGCTATTCCGGCAAAGAACGAGATG	CCACCGGGTTGTA
tccC3-W14	(1849)	TATAAAACTATC	CGTTATTTCAGGCAAAGAGCGGGATG	CCACCGGGCTATA
tccC4-W14	(1849)	TACAAAATCCTC	CGTTACTCAGGTAAAGAACGCGATG	CTACCGGGCTCTA
tccC5-W14	(1822)	TATAAAACCATT	CGTTATTCTGGTAAAGAGCGGGATG	TTACCGGGCTGTA
xptB1-Xwi	(1855)	TACAAAACCGTG	CGTTATTCTGGCAAAGAGCGGGATG	CAACAGGGTTGTA

SB213

Fig. 14B